
Spatiotemporal Reconstruction of the Human Blastocyst by Single-Cell Gene-Expression Analysis Informs Induction of Naive Pluripotency.

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Public Summary:

There are three cell lineages in the blastocyst stage of human embryo development: trophectoderm, primitive endoderm, and epiblast. Due limited access to human embryos, we have limited understanding of how each lineage come about. We examine the gene expression of 241 single cells from early to late human blastocyst to tease out the gene expression changes. We identify role for MCRC1, TET1, and THAP11 in epiblast formation and their ability to induce naïve pluripotency in vitro. Our method demonstrates that single cell gene expression analysis will further the understanding of human stem cell biology.

Scientific Abstract:

Human preimplantation embryo development involves complex cellular and molecular events that lead to the establishment of three cell lineages in the blastocyst: trophectoderm, primitive endoderm, and epiblast. Owing to limited resources of biological specimens, our understanding of how the earliest lineage commitments are regulated remains narrow. Here, we examined gene expression in 241 individual cells from early and late human blastocysts to delineate dynamic gene-expression changes. We distinguished all three lineages and further developed a 3D model of the inner cell mass and trophectoderm in which individual cells were mapped into distinct expression domains. We identified in silico precursors of the epiblast and primitive endoderm lineages and revealed a role for MCRC1, TET1, and THAP11 in epiblast formation and their ability to induce naïve pluripotency in vitro. Our results highlight the potential of single-cell gene-expression analysis in human preimplantation development to instruct human stem cell biology.

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